



IFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/940,673B

DATE: 09/16/2004

TIME: 11:44:05

Input Set : A:\22311040.app

Output Set: N:\CRF4\09162004\I940673B.raw

3 <110> APPLICANT: GORSKI, DAVID H.
 4 WALSH, KENNETH
 6 <120> TITLE OF INVENTION: GROWTH ARREST HOMEBOX GENE
 8 <130> FILE REFERENCE: 22311/04015
 10 <140> CURRENT APPLICATION NUMBER: 09/940,673B
 11 <141> CURRENT FILING DATE: 2001-08-27
 13 <150> PRIOR APPLICATION NUMBER: 09/078,465
 14 <151> PRIOR FILING DATE: 1998-05-14
 16 <150> PRIOR APPLICATION NUMBER: 08/203,532
 17 <151> PRIOR FILING DATE: 1994-02-24
 19 <160> NUMBER OF SEQ ID NOS: 19
 21 <170> SOFTWARE: PatentIn Ver. 2.1
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 2244
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Rattus sp.
 28 <220> FEATURE:
 29 <221> NAME/KEY: CDS
 30 <222> LOCATION: (197)..(1105)
 32 <400> SEQUENCE: 1
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 35 ctgctcaaac ccgcgcggct tttacattag gaggtagtgg gggagagtcc taggatttct 120
 37 agtgaaaagt gacagcgctt ggtggacttt gggaccttcg tgaagtcttc tgcttgggaag 180
 39 ctgagacttg catgcc atg gaa cac ccc ctc ttt ggc tgc ctg cgc agc ccc 232
 40 Met Glu His Pro Leu Phe Gly Cys Leu Arg Ser Pro
 41 1 5 10
 43 cac gcc aca gcg caa ggc ttg cac ccc ttc tcg cag tct tct ctg gcc 280
 44 His Ala Thr Ala Gln Gly Leu His Pro Phe Ser Gln Ser Ser Leu Ala
 45 15 20 25
 47 ctc cat gga aga tct gac cac atg tcc tac ccc gaa ctc tcc aca tct 328
 48 Leu His Gly Arg Ser Asp His Met Ser Tyr Pro Glu Leu Ser Thr Ser
 49 30 35 40
 51 tcc tcg tct tgc ata atc gcg gga tac ccc aat gag gag ggc atg ttt 376
 52 Ser Ser Ser Cys Ile Ile Ala Gly Tyr Pro Asn Glu Glu Gly Met Phe
 53 45 50 55 60
 55 gcc agc cag cat cac agg ggg cac cac cac cac cac cac cac cat 424
 56 Ala Ser Gln His His Arg Gly His His His His His His His His
 57 65 70 75
 59 cac cac cac cag cag cag cag cac cag gct ctg caa agc aac tgg cac 472
 60 His His His Gln Gln Gln Gln His Gln Ala Leu Gln Ser Asn Trp His
 61 80 85 90
 63 ctc ccg cag atg tcc tcc ccg cca agc gcg gcc cgg cac agc ctt tgc 520
 64 Leu Pro Gln Met Ser Ser Pro Pro Ser Ala Ala Arg His Ser Leu Cys

(pg. 6)

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65          95          100          105
67 ctg cag cct gat tcc gga ggg ccc ccg gag ctg ggg agc agc cct ccg 568
68 Leu Gln Pro Asp Ser Gly Gly Pro Pro Glu Leu Gly Ser Ser Pro Pro
69      110          115          120
71 gtc ctg tgc tcc aac tct tct agc ctg ggc tcc agc acc ccg acc gga 616
72 Val Leu Cys Ser Asn Ser Ser Ser Leu Gly Ser Ser Thr Pro Thr Gly
73 125          130          135          140
75 gcc gcg tgc gca cca agg gat tat ggc cgt caa gcg ctg tca ccc gca 664
76 Ala Ala Cys Ala Pro Arg Asp Tyr Gly Arg Gln Ala Leu Ser Pro Ala
77      145          150          155
79 gaa gtg gag aag aga agt ggc agc aaa aga aaa agc gac agt tca gat 712
80 Glu Val Glu Lys Arg Ser Gly Ser Lys Arg Lys Ser Asp Ser Ser Asp
81      160          165          170
83 tcc cag gaa gga aat tac aag tca gaa gtg aac agc aaa cct agg aag 760
84 Ser Gln Glu Gly Asn Tyr Lys Ser Glu Val Asn Ser Lys Pro Arg Lys
85      175          180          185
87 gaa aga aca gct ttc acc aaa gag caa atc aga gaa ctt gag gca gag 808
88 Glu Arg Thr Ala Phe Thr Lys Glu Gln Ile Arg Glu Leu Glu Ala Glu
89      190          195          200
91 ttc gcc cat cat aac tat ctg acc aga ctg aga aga tat gag ata gcg 856
92 Phe Ala His His Asn Tyr Leu Thr Arg Leu Arg Arg Tyr Glu Ile Ala
93 205          210          215          220
95 gtg aac cta gac ctc act gaa aga cag gtg aaa gtg tgg ttc cag aac 904
96 Val Asn Leu Asp Leu Thr Glu Arg Gln Val Lys Val Trp Phe Gln Asn
97      225          230          235
99 agg aga atg aag tgg aag cgg gtc aag ggg gga caa caa gga gct gca 952
100 Arg Arg Met Lys Trp Lys Arg Val Lys Gly Gly Gln Gln Gly Ala Ala
101      240          245          250
103 gcc cga gaa aag gaa ctg gtg aat gtg aaa aag gga aca ctt ctt cca 1000
104 Ala Arg Glu Lys Glu Leu Val Asn Val Lys Lys Gly Thr Leu Leu Pro
105      255          260          265
107 tca gag ctg tca gga att ggt gca gcc acc ctc cag cag aca ggg gac 1048
108 Ser Glu Leu Ser Gly Ile Gly Ala Ala Thr Leu Gln Gln Thr Gly Asp
109      270          275          280
111 tca cta gca aat gac gac agt cgc gat agt gac cac agc tct gag cac 1096
112 Ser Leu Ala Asn Asp Asp Ser Arg Asp Ser Asp His Ser Ser Glu His
113 285          290          295          300
115 gca cac tta tgatacatc agagaccagc tccgttctca ggaaagcacc 1145
116 Ala His Leu
118 attgtgatgg caaatctcac ccaaacatcg tttacatggc agatgactgt ggcagtgttg 1205
120 cttaatatata ttaaacgcag gcatctcaag tctgtttctc atgattgata gaaggtttac 1265
122 actaagtgcc tcttattgaa gatgcttcca cagtgaatg ggagaaagtg aacatatcta 1325
124 aatatacttg ttccttatat gacagagagg gagatgaatg tttgctttgg cttgactga 1385
126 aaattaaatt gctaccaaga gcaaactcgg taagacattt tgactcaagt tgtctccaga 1445
128 gtgaagatgt tatagaaatg ctttgaacat tccagttgta ccaggtcacg tgtgtgacac 1505
130 tgggcaggta tttgcttttg cttgactga aacttaaaact gctatcaagt taacctatga 1565
132 aatagtttat cttgaacagc cacagtgcct gaaatcacca agtggatata aaatgaactg 1625
134 aaattctgta tatattactc ctaagtcatt ttcctgtctt cactaatttt agcaaagtga 1685
136 ttcataattag ctgatgaaaa taggctttcc cgtggacaaa tgcagccagc ttcttgatt 1745

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138 ttatacatatt tttttgtcag tcagagacat cagtatgtgc ttacttgtgt tcaagtagag 1805
140 gaaatgcagt agagtctgat aggacatatt cttggtacca cagacaaaac aaatcttctg 1865
142 ttgcattgac tatcaactgc tgcagataca ttagagaaca cacctagccc ccctccagcc 1925
144 tccctctgtt atcgctcgaa gacattagcg tcataggcaa gtagttacct tgccaaatga 1985
146 gtcttgtgtg gcagatgtct gattttgtat ctttaaaactg ttaatggtat gtgtctgctt 2045
148 cagttaacag ggaaaaagat ttcttctca ttgtttatga tacaaaaccc aagtgcacaa 2105
150 caaagctagt tcttcaaggg atagatgaga aactgaatgt ctgacaagta gactcagcga 2165
152 aaatacatta tttttcagag gctgtgtatt catgcagtac aagtccttgt attttgtaaa 2225
154 aaaaaaagtt aaataaatg                                     2244
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158 <211> LENGTH: 303
159 <212> TYPE: PRT
160 <213> ORGANISM: Rattus sp.
162 <400> SEQUENCE: 2
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164 1 5 10 15
166 Gln Gly Leu His Pro Phe Ser Gln Ser Ser Leu Ala Leu His Gly Arg
167 20 25 30
169 Ser Asp His Met Ser Tyr Pro Glu Leu Ser Thr Ser Ser Ser Cys
170 35 40 45
172 Ile Ile Ala Gly Tyr Pro Asn Glu Glu Gly Met Phe Ala Ser Gln His
173 50 55 60
175 His Arg Gly His His His His His His His His His His His His Gln
176 65 70 75 80
178 Gln Gln Gln His Gln Ala Leu Gln Ser Asn Trp His Leu Pro Gln Met
179 85 90 95
181 Ser Ser Pro Pro Ser Ala Ala Arg His Ser Leu Cys Leu Gln Pro Asp
182 100 105 110
184 Ser Gly Gly Pro Pro Glu Leu Gly Ser Ser Pro Pro Val Leu Cys Ser
185 115 120 125
187 Asn Ser Ser Ser Leu Gly Ser Ser Thr Pro Thr Gly Ala Ala Cys Ala
188 130 135 140
190 Pro Arg Asp Tyr Gly Arg Gln Ala Leu Ser Pro Ala Glu Val Glu Lys
191 145 150 155 160
193 Arg Ser Gly Ser Lys Arg Lys Ser Asp Ser Ser Asp Ser Gln Glu Gly
194 165 170 175
196 Asn Tyr Lys Ser Glu Val Asn Ser Lys Pro Arg Lys Glu Arg Thr Ala
197 180 185 190
199 Phe Thr Lys Glu Gln Ile Arg Glu Leu Glu Ala Glu Phe Ala His His
200 195 200 205
202 Asn Tyr Leu Thr Arg Leu Arg Arg Tyr Glu Ile Ala Val Asn Leu Asp
203 210 215 220
205 Leu Thr Glu Arg Gln Val Lys Val Trp Phe Gln Asn Arg Arg Met Lys
206 225 230 235 240
208 Trp Lys Arg Val Lys Gly Gly Gln Gln Gly Ala Ala Ala Arg Glu Lys
209 245 250 255
211 Glu Leu Val Asn Val Lys Lys Gly Thr Leu Leu Pro Ser Glu Leu Ser
212 260 265 270
214 Gly Ile Gly Ala Ala Thr Leu Gln Gln Thr Gly Asp Ser Leu Ala Asn

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215          275          280          285
217 Asp Asp Ser Arg Asp Ser Asp His Ser Ser Glu His Ala His Leu
218          290          295          300
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223 <211> LENGTH: 941
224 <212> TYPE: DNA
225 <213> ORGANISM: Homo sapiens
227 <220> FEATURE:
228 <221> NAME/KEY: CDS
229 <222> LOCATION: (33)..(938)
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233                               Met Glu His Pro Leu Phe Gly
234                               1           5
236 tgc ctg cgc agc cct cac gcc acg gcg caa ggc ttg cac ccg ttc tcc 101
237 Cys Leu Arg Ser Pro His Ala Thr Ala Gln Gly Leu His Pro Phe Ser
238          10          15          20
240 caa tcc tct ctc gcc ctc cat gga aga tct gac cat atg tct tac ccc 149
241 Gln Ser Ser Leu Ala Leu His Gly Arg Ser Asp His Met Ser Tyr Pro
242          25          30          35
244 gag ctc tct act tct tcc tca tct tgc ata atc gcg gga tac ccc aac 197
245 Glu Leu Ser Thr Ser Ser Ser Ser Cys Ile Ile Ala Gly Tyr Pro Asn
246 40          45          50          55
248 gaa gag gac atg ttt gcc agc cag cat cac agg ggg cac cac cac cac 245
249 Glu Glu Asp Met Phe Ala Ser Gln His His Arg Gly His His His His
250          60          65          70
252 cac cac cac cat cac cac cat cag cag cag cag cac cag gct ctg caa 293
253 His His His His His His His Gln Gln Gln Gln His Gln Ala Leu Gln
254          75          80          85
256 acc aac tgg cac ctc ccg cag atg tct tcc cca ccg agt gcg gct cgg 341
257 Thr Asn Trp His Leu Pro Gln Met Ser Ser Pro Pro Ser Ala Ala Arg
258          90          95          100
260 cat agc ctc tgc ctc cag ccc gac tct gga ggg ccc cca gag ttg ggg 389
261 His Ser Leu Cys Leu Gln Pro Asp Ser Gly Gly Pro Pro Glu Leu Gly
262          105          110          115
264 agc agc ccg ccc gtc ctg tgc tcc aac tct tcc agc ttg ggc tcc agc 437
265 Ser Ser Pro Pro Val Leu Cys Ser Asn Ser Ser Ser Leu Gly Ser Ser
266 120          125          130          135
268 acc ccg act ggg gcc gcg tgc gcg ccg ggg gac tac ggc cgc cag gca 485
269 Thr Pro Thr Gly Ala Ala Cys Ala Pro Gly Asp Tyr Gly Arg Gln Ala
270          140          145          150
272 ctg tca cct gcg gag gcg gag aag cga agc ggc ggc aag agg aaa agc 533
273 Leu Ser Pro Ala Glu Ala Glu Lys Arg Ser Gly Gly Lys Arg Lys Ser
274          155          160          165
276 gac agc tca gac tcc cag gaa gga aat tac aag tca gaa gtc aac agc 581
277 Asp Ser Ser Asp Ser Gln Glu Gly Asn Tyr Lys Ser Glu Val Asn Ser
278          170          175          180
280 aaa ccc agg aaa gaa agg aca gca ttt acc aaa gag caa atc aga gaa 629
281 Lys Pro Arg Lys Glu Arg Thr Ala Phe Thr Lys Glu Gln Ile Arg Glu

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Input Set : A:\22311040.app

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282      185      190      195
284 ctt gaa gca gaa ttt gcc cat cat aat tat ctc acc aga ctg agg cga 677
285 Leu Glu Ala Glu Phe Ala His His Asn Tyr Leu Thr Arg Leu Arg Arg
286 200      205      210      215
288 tac gag ata gca gtg aat ctg gat ctc act gaa aga cag gta aaa gtc 725
289 Tyr Glu Ile Ala Val Asn Leu Asp Leu Thr Glu Arg Gln Val Lys Val
290      220      225      230
292 tgg ttc caa aac agg cgg atg aag tgg aag agg gta aag ggt gga cag 773
293 Trp Phe Gln Asn Arg Arg Met Lys Trp Lys Arg Val Lys Gly Gly Gln
294      235      240      245
296 caa gga gct gcg gct cgg gaa aag gaa ctg gtg aat gtg aaa aag gga 821
297 Gln Gly Ala Ala Ala Arg Glu Lys Glu Leu Val Asn Val Lys Lys Gly
298      250      255      260
300 aca ctt ctc cca tca gag ctg tcg gga att ggt gca gcc acc ctc cag 869
301 Thr Leu Leu Pro Ser Glu Leu Ser Gly Ile Gly Ala Ala Thr Leu Gln
302      265      270      275
304 caa aca ggg gac tct ata gca aat gaa gac agt cac gac agt gac cac 917
305 Gln Thr Gly Asp Ser Ile Ala Asn Glu Asp Ser His Asp Ser Asp His
306 280      285      290      295
308 agc tca gag cac gcc cac ctc tga 941
309 Ser Ser Glu His Ala His Leu
310      300
313 <210> SEQ ID NO: 4
314 <211> LENGTH: 302
315 <212> TYPE: PRT
316 <213> ORGANISM: Homo sapiens
318 <400> SEQUENCE: 4
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322 Gln Gly Leu His Pro Phe Ser Gln Ser Ser Leu Ala Leu His Gly Arg
323      20      25      30
325 Ser Asp His Met Ser Tyr Pro Glu Leu Ser Thr Ser Ser Ser Cys
326      35      40      45
328 Ile Ile Ala Gly Tyr Pro Asn Glu Glu Asp Met Phe Ala Ser Gln His
329      50      55      60
331 His Arg Gly His His His His His His His His His His Gln Gln
332 65      70      75      80
334 Gln Gln His Gln Ala Leu Gln Thr Asn Trp His Leu Pro Gln Met Ser
335      85      90      95
337 Ser Pro Pro Ser Ala Ala Arg His Ser Leu Cys Leu Gln Pro Asp Ser
338      100      105      110
340 Gly Gly Pro Pro Glu Leu Gly Ser Ser Pro Pro Val Leu Cys Ser Asn
341      115      120      125
343 Ser Ser Ser Leu Gly Ser Ser Thr Pro Thr Gly Ala Ala Cys Ala Pro
344      130      135      140
346 Gly Asp Tyr Gly Arg Gln Ala Leu Ser Pro Ala Glu Ala Glu Lys Arg
347 145      150      155      160
349 Ser Gly Gly Lys Arg Lys Ser Asp Ser Ser Asp Ser Gln Glu Gly Asn
350      165      170      175

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/940,673B

DATE: 09/16/2004
TIME: 11:44:06

Input Set : A:\22311040.app
Output Set: N:\CRF4\09162004\I940673B.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 6,21,24
Seq#:6; N Pos. 4,10

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/940,673B

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Input Set : A:\22311040.app

Output Set: N:\CRF4\09162004\I940673B.raw

L:403 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:426 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0